

**Marked Changes**

Amend claim 1 as follows:

1. (amended) A method of analyzing a plurality of target nucleic acid sequences in a sample, the method comprising:

providing, for each target nucleic acid sequence to be analyzed, at least one probe/primer molecule which probe/primer molecule includes a region of sequence substantially complementary to a sequence in the target nucleic acid sequence and a region that is not located at either terminus of the probe/primer molecule and which includes a capture tag sequence;

forming a reaction mixture which includes the probe/primer molecules and the target sequences under conditions such that, if a probe/primer molecule specific for a target sequence and that target sequence are both present, one or a plurality of derivative molecules having a capture tag at one or both its 3' or 5' termini, of the probe/primer molecule specific for the target sequence, is generated; and

evaluating the presence of one or more derivative molecules, each derivative molecule indicating a target nucleic acid sequence in the sample, thereby analyzing the plurality of target nucleic acid sequences in the sample.